RAW SEQUENCE LISTING PATENT APPLICATION US/08/436,265

.TIME: 14:53:04

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This Raw Listing contains the General Information Section and up to the first 5 pages.

TERED 1 SEQUENCE LISTING 2 3 (1) General Information: 4 5 (i) APPLICANTS: Miyazono, Kohei; Dijke, Peter Ten; 6 Franzen, Petra; Yamashita, Hidetoshi; Heldin, Carl-Henrik 7 (ii) TITLE OF INVENTION: Activin Receptor-Like Kinase, Proteins 8 9 Having Serine Threonine Kinase Domains And Their Use 10 11 (iii) NUMBER OF SEQUENCES: 12 (iv) CORRESPONDENCE ADDRESS: 13 14 (A) ADDRESSEE: Felfe & Lynch 15 (B) STREET: 805 Third Avenue 16 (C) CITY: New York City 17 (D) STATE: New York 18 (F) ZIP: 10022 19 20 (V) COMPUTER READABLE FORM: (A) MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage 21 22 (B) COMPUTER: IBM 23 (C) OPERATING SYSTEM: PC-DOS 24 (D) SOFTWARE: Wordperfect 25 26 (vi) CURRENT APPLICATION DATA: 27 (A) APPLICATION NUMBER: 08/436,265 28 (B) FILING DATE: 30-October-1995 01/29 (C) CLASSIFICATION: 514 30 31 (vii) PRIOR APPLICATION DATA: 32 (A) APPLICATION NUMBER: PCT/GB93/02367 33 (B) FILING DATE: 17-November-1993 34 35 (vii) PRIOR APPLICATION DATA: 36 (A) APPLICATION NUMBER: 9224057.1 37 (B) FILING DATE: 17-November-1992 38 39 (vii) PRIOR APPLICATION DATA: 40 (A) APPLICATION NUMBER: 9304677.9 (B) FILING DATE: 8-March-1993 41 42 43 (vii) PRIOR APPLICATION DATA: 44 (A) APPLICATION NUMBER: 9304680.3 (B) FILING DATE: 8-March-1993 45 46

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RAW SEQUENCE LISTING PATENT APPLICATION US/08/436,265

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47	(vii) PRIOR APPLICATION DATA:	
48	(A) APPLICATION NUMBER: 9311047.6	
49	(B) FILING DATE: 28-May-1993	
50		
51	(vii) PRIOR APPLICATION DATA:	
52	(A) APPLICATION NUMBER: 9313763.6	
53	(B) FILING DATE: 2-July-1993	
54		
55	(vii) PRIOR APPLICATION DATA:	
56	(A) APPLICATION NUMBER: 9136099.2	
57	(B) FILING DATE: 3-August-1993	
58	(-//) PRIOR ARRIVANTON PARA	
59	(vii) PRIOR APPLICATION DATA:	
60	(A) APPLICATION NUMBER: 9321344.5	
61	(B) FILING DATE: 15-October-1993	
62		
63	(viii) ATTORNEY/AGENT INFORMATION:	
64	(A) NAME: Kohlei, Vineet	
65	(B) REGISTRATION NUMBER: 37,003	
66	(C) REFERENCE/DOCKET NUMBER: LUD 5298	
67	(land management and	
68	(ix) TELECOMMUNICATION INFORMATION:	
69	(A) TELEPHONE: (212) 688-9200	
70	(B) TELEFAX: (212) 838-3884	
71		
72		
73	(2) THEODIAMICAL BOD GEO TO NO. 1.	
7 4	(2) INFORMATION FOR SEQ ID NO: 1:	
75 76	(i) SEQUENCE CHARACTERISTICS:	
70 77	(A) LENGTH: 1984 base pairs	
7 / 78	(B) TYPE: nucleic acid	
78 79	(C) STRANDEDNESS: unknown	
	(D) TOPOLOGY: linear	
80 81	(ii) MOLECULE TYPE: cDNA	
82	(iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO	
83	(v) FRAGMENT TYPE: internal	
84	· •	
85	(vi) ORIGINAL SOURCE:	
86	(A) ORGANISM: Homo sapiens (ix) FEATURE:	
87	(A) NAME/KEY: CDS	
88	(B) LOCATION: 2831791	
89	(xi) SEOUENCE DESCRIPTION: SEO ID NO: 1:	
90	(XI) SEQUENCE DESCRIPTION: SEQ ID NO. I.	
91	AGGAAACGGT TTATTAGGAG GGAGTGGTGG AGCTGGGCCA GGCAGGAAGA CGCTGGAATA	60
92	ACCIDENTAL CONTINUE C	00
93	AGAAACATTT TTGCTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC	120
94	AGAMACATIT TIGGTCCAGC CCCCATCCCA GTCCCGGGAG GCTGCCGCGC CAGCTGCGCC	120
95	GAGCGAGCCC CTCCCCGGCT CCAGCCCGGT CCGGGGCCGC GCCGGACCCC AGCCCGCCGT	180
96	SACCORSCIC CICCOGGCI CONSCICUGI COGGGGCCGC GCCGGACCCC AGCCCGCCGI	100
97	CCAGCGCTGG CGGTGCAACT GCGGCCGCGC GGTGGAGGGG AGGTGGCCCC GGTCCGCCGA	240
98	CONCUENT COOLOGIC COOLOGICO COLOGICO CO	240
99	AGGCTAGCGC CCCGCCACCC GCAGAGCGGG CCCAGAGGGA CC ATG ACC TTG GGC	294

PAGE: 3 RAW SEQUENCE LISTING DATE: 03/12/97 PATENT APPLICATION US/08/436,265 TIME: 14:53:10

Met Thr Leu Gly															IN	PUT	SET:	S16122.raw
103	100												ì	Met '	_			
101 Ser Pro Arg Lys Gly Leu Leu Met Leu Met Ala Leu Val Arg Clo Clo	101													1				
104 Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala Leu Val Thr Gln 20	102																	
105	103	TCC	CCC	AGG	AAA	GGC	CTT	CTG	ATG	CTG	CTG	ATG	GCC	TTG	GTG	ACC	CAG	342
106	104	Ser	Pro	Arg	Lys	Gly	Leu	Leu	Met	Leu	Leu	Met	Ala	Leu	Val	Thr	Gln	
107 GGA GAC CCT GTG AAG CCG TCT CGG GGC CCG CTG GTG ACC TGC ACG TGT CGG GGA GAG CAG CTG TGT CAG GGA GAG CAG CTG TGT CAG GGA GAG CAG CAG CAG AGAG CAG CAG CA	105	5					10					15					20	
108	106																	
109	107	GGA	GAC	CCT	GTG	AAG	CCG	TCT	CGG	GGC	CCG	CTG	GTG	ACC	TGC	ACG	TGT	390
110	108	Gly	Asp	Pro	Val	Lys	Pro	Ser	Arg	Gly	Pro	Leu	Val	Thr	Cys	Thr	Cys	
111						25					30					35		
113	110																	
113																		438
114		Glu	Ser	Pro	His	Cys	Lys	Gly	Pro	Thr	Cys	Arg	Gly	Ala	Trp	Cys	Thr	
115	113				40					45					50			
116																		
116																		486
118		Val	Val		Val	Arg	Glu	Glu	Gly	Arg	His	Pro	Gln	Glu	His	Arg	Gly	
119				55					60					65				
120																		
121																		534
122		Cys		Asn	Leu	His	Arg		Leu	Cys	Arg	СТĀ	_	Pro	Thr	Glu	Phe	
123			70					75					80					
124																		
125																		582
126			Asn	HIS	Tyr	cys	_	Asp	ser	HIS	Leu	_	Asn	HIS	Asn	vaı		
127		85					90					95					100	
128		аша	аша	ama	a.a	000	3.00	CIR R	aam	aam	maa	a a a	a.a	000	003	303	G N III	620
129																		630
130 131 GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC TTG CTG GCC CTG 678 132 Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala Leu Leu Ala Leu 133 120 125 130 130 130 131 130 131 130 130 131 130 131 130 131 130 131 130 131 131 135 140 145 145 145 135 140 145 145 138 139 AAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG 774 140 Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu 141 150 155 160 155 160 160 142 144 Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser 145 165 170 170 175 180 146 147 GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG 870 148 Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg 149 185 190 195 150 151 ACA GTG GCA GGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG AAA GGC CGC 918 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG AAA GGC CGC 918 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG AAA GGC CGC 918 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG AAA GGC CGC 918 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GTG GGA AAA GGC CGC 918 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GTG GGA AAA GGC CGC 918 151 15		Leu	vaı	Leu	GIU		THE	GIII	PIO	PIO		GIU	GIII	PIO	СТУ		ASP	
131 GGC CAG CTG GCC CTG ATC CTG GGC CCC GTG CTG GCC CTG GCC CTG CTG GCC CTG GCC CTG GCC GTG GTG						105					110					113		
132		age	CAG	ርጥር	acc	כיזים	አሞሮ	СТС	aac	ccc	GTG.	CTG	acc	ጥጥር	משמ	מפפ	CTC	678
133																		070
134 135		GLY	GTII	nea		пец	116	Беа	СТУ		Vai	пеа	AIG	neu		АТа	пец	
135					120					123					130			
136		GTG	GCC	ста	сст	GTC	СТС	GGC	ста	TGG	САТ	GTC	CGA	CGG	AGG	CAG	GAG	726
137																		, 20
138 139		,			,			1					9		9			
139 AAG CAG CAG CGT GGC CTG CAC AGC GAG CTG GGA GAG TCC AGT CTC ATC CTG 774 140 Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu 141 141 150 155 160 142 143 AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT 822 144 Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser 145 145 165 170 175 180 146 147 GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG 870 148 Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg 195 149 185 190 195 150 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918																		
140 Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser Ser Leu Ile Leu 141 150 155 160 142 143 AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT 822 144 Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser 145 145 165 170 175 180 146 147 GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG 870 148 Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg 195 149 185 190 195 150 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918		AAG	CAG	CGT	GGC	CTG	CAC	AGC	GAG	CTG	GGA	GAG	TCC	AGT	CTC	ATC	CTG	774
141 150 155 160 142 143 AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT 822 144 Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser 145 145 165 170 175 180 146 147 GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG 870 148 Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg 149 185 190 195 150 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918	140																	
143 AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT 822 144 Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser 145 165 170 175 180 146 147 GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG 870 148 Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg 195 149 185 190 195 150 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918		-			-						-							
143 AAA GCA TCT GAG CAG GGC GAC ACG ATG TTG GGG GAC CTC CTG GAC AGT 822 144 Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser 145 165 170 175 180 146 147 GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG 870 148 Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg 195 149 185 190 195 150 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918	142																	
144 Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp Leu Leu Asp Ser 145 165 170 175 180 146 147 GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG 870 148 Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg 195 149 185 190 195 150 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918		AAA	GCA	TCT	GAG	CAG	GGC	GAC	ACG	ATG	TTG	GGG	GAC	CTC	CTG	GAC	AGT	822
145 165 170 175 180 146 146 147 GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG 870 148 Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg 149 149 185 190 195 150 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918	144	Lys	Ala	Ser	Glu	Gln	Gly	Asp	Thr	Met	Leu	Gly	Asp	Leu	Leu	Asp	Ser	
147 GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG 870 148 Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg 149 185 190 195 150 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918	145	_					_	-				_	-			-		
147 GAC TGC ACC ACA GGG AGT GGC TCA GGG CTC CCC TTC CTG GTG CAG AGG 870 148 Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe Leu Val Gln Arg 149 185 190 195 150 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918	146																	
149 185 190 195 150 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918		GAC	TGC	ACC	ACA	GGG	AGT	GGC	TCA	GGG	CTC	CCC	TTC	CTG	GTG	CAG	AGG	870
149 185 190 195 150 151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918	148	Asp	Cys	Thr	Thr	Gly	Ser	Gly	Ser	Gly	Leu	Pro	Phe	Leu	Val	Gln	Arg	
151 ACA GTG GCA CGG CAG GTT GCC TTG GTG GAG TGT GTG GGA AAA GGC CGC 918	149	_	-			_		_		_							-	
	150																	
152 Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val Gly Lys Gly Arg	151	ACA	GTG	GCA	CGG	CAG	GTT	GCC	TTG	GTG	GAG	TGT	GTG	GGA	AAA	GGC	CGC	918
	152	Thr	Val	Ala	Arg	Gln	Val	Ala	Leu	Val	Glu	Cys	Val	Gly	Lys	Gly	Arg	

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153				200					205					210				
154																		
155	TAT	GGC	GAA	GTG	TGG	CGG	GGC	TTG	TGG	CAC	GGT	GAG	AGT	GTG	GCC	GTC	966	
156	Tyr	Gly	Glu	Val	Trp	Arg	Gly	Leu	Trp	His	Gly	Glu	Ser	Val	Ala	Val		
157			215					220					225					
158														•				
159	AAG	ATC	TTC	TCC	TCG	AGG	GAT	GAA	CAG	TCC	TGG	TTC	CGG	GAG	ACT	GAG	1014	
160	Lys	Ile	Phe	Ser	Ser	Arg	Asp	Glu	Gln	Ser	Trp	Phe	Arg	Glu	Thr	Glu		
161	_	230				_	235				_	240	_					
162																		
163	ATC	TAT	AAC	ACA	GTA	TTG	CTC	AGA	CAC	GAC	AAC	ATC	CTA	GGC	TTC	ATC	1062	
164	Ile	Tyr	Asn	Thr	Val	Leu	Leu	Arg	His	Asp	Asn	Ile	Leu	Gly	Phe	Ile		
165	245					250		_		_	255			_		260		
166																		
167	GCC	TCA	GAC	ATG	ACC	TCC	CGC	AAC	TCG	AGC	ACG	CAG	CTG	TGG	CTC	ATC	1110	
168						Ser												
169			_		265		_			270				-	275			
170																		
171	ACG	CAC	TAC	CAC	GAG	CAC	GGC	TCC	CTC	TAC	GAC	TTT	CTG	CAG	AGA	CAG	1158	
172	Thr	His	Tyr	His	Glu	His	Gly	Ser	Leu	Tyr	Asp	Phe	Leu	Gln	Arg	Gln		
173			_	280			-		285	-	-			290	_			
174																		
175	ACG	CTG	GAG	CCC	CAT	CTG	GCT	CTG	AGG	CTA	GCT	GTG	TCC	GCG	GCA	TGC	1206	
176	Thr	Leu	Glu	Pro	His	Leu	Ala	Leu	Arg	Leu	Ala	Val	Ser	Ala	Ala	Cys		
177			295					300	_				305			-		
178																		
179	GGC	CTG	GCG	CAC	CTG	CAC	GTG	GAG	ATC	TTC	GGT	ACA	CAG	GGC	AAA	CCA	1254	
180	Gly	Leu	Ala	His	Leu	His	Val	Glu	Ile	Phe	Gly	Thr	Gln	Gly	Lys	Pro		
181		310					315				_	320		_	_			
182																		
183	GCC	ATT	GCC	CAC	CGC	GAC	TTC	AAG	AGC	CGC	AAT	GTG	CTG	GTC	AAG	AGC	1302	
184	Ala	Ile	Ala	His	Arg	Asp	Phe	Lys	Ser	Arg	Asn	Val	Leu	Val	Lys	Ser		
185	325					330				_	335				_	340		
186																		
187	AAC	CTG	CAG	TGT	TGC	ATC	GCC	GAC	CTG	GGC	CTG	GCT	GTG	ATG	CAC	TCA	1350	
188	Asn	Leu	Gln	Cys	Cys	Ile	Ala	Asp	Leu	Gly	Leu	Ala	Val	Met	His	Ser		
189					345					350					355			
190																		
191	CAG	GGC	AGC	GAT	TAC	CTG	GAC	ATC	GGC	AAC	AAC	CCG	AGA	GTG	GGC	ACC	1398	
192	Gln	Gly	Ser	Asp	Tyr	Leu	Asp	Ile	Gly	Asn	Asn	Pro	Arg	Val	Gly	Thr		
193				360					365					370				
194																		
195	AAG	CGG	TAC	ATG	GCA	CCC	GAG	GTG	CTG	GAC	GAG	CAG	ATC	CGC	ACG	GAC	1446	
196	Lys	Arg	Tyr	Met	Ala	Pro	Glu	Val	Leu	Asp	Glu	Gln	Ile	Arg	Thr	Asp		
197			375					380					385					
198																		
199	TGC	TTT	GAG	TCC	TAC	AAG	TGG	ACT	GAC	ATC	TGG	GCC	$\mathbf{T}\mathbf{T}\mathbf{T}$	GGC	CTG	GTG	1494	
200	Cys	Phe	Glu	Ser	Tyr	Lys	Trp	Thr	Asp	Ile	Trp	Ala	Phe	Gly	Leu	Val		
201	-	390			-		395					400						
202																		
203	CTG	TGG	GAG	ATT	GCC	CGC	CGG	ACC	ATC	GTG	AAT	GGC	ATC	GTG	GAG	GAC	1542	
204	Leu	Trp	Glu	Ile	Ala	Arg	Arg	Thr	Ile	Val	Asn	Gly	Ile	Val	Glu	Asp		
205	405					410	-				415	-				420		

PAGE: 5 RAW SEQUENCE LISTING PATENT APPLICATION US/08/436,265

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TAT AGA CCA CCC TTC TAT GAT GTG TGT GTG CCC AAT GAC CCC AGC TTT GAG															II!	<i>NPUT</i>	SET: S1612	2.raw
Type Arg Pro Pro Pro Pro Pro Pro Yasp Val Val Pro Asn Asp Pro Ser Phe Glu 435 435 435 435 436 436 435 436 435 436 435 436 435 436 435 436 435 436 43																		
209 210 211 212 213 214 215 216 217 218 219 219 219 210 211 210 211 211 212 212 213 214 214 215 214 215 216 217 218 218 219 219 219 210 210 211 210 211 211 212 213 214 214 215 216 217 218 217 218 219 219 219 219 219 219 219 219 219 219																		1590
210		ıyı	ALG	PLO	PIO		ıyı	АБР	Val	Val		ASII	АБР	PIO	Ser		GIU	
Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr Pro Thr Tle Pro																		
ALC COG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG ATG ASA ATG Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met	211	GAC	ATG	AAG	AAG	GTG	GTG	TGT	GTG	GAT	CAG	CAG	ACC	CCC	ACC	ATC	CCT	1638
214 215 AAC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG 216 ASN ATG Leu Ala Ala Asp Pro Val Leu Ser Gly Leu Ala Gln Met Met 217 455 460 465 218 219 CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG 1734 220 Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu Thr Ala Leu Arg 221 470 475 480 222 ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA 1782 223 ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA 1782 224 Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys 225 485 490 500 226 227 GTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC 1831 228 Val Ile Gln 229 230 TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG 1891 231 232 TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC AGCCAAAAAT 1951 233 234 ACAGCTGGGC TGAAACCTGA AAAAAAAAAAAA AAA 1984 235 (2) INFORMATION FOR SEQ ID NO: 2: 236 (3) SEQUENCE CHARACTERISTICS: 237 (2) INFORMATION FOR SEQ ID NO: 2: 238 (2) INFORMATION FOR SEQ ID NO: 2: 249 (3) TYPE: amino acid 240 (3) TYPE: amino acid 241 (3) TYPE: amino acid 242 (1) TOPOLOGY: linear 243 (ii) MOLECULE TYPE: protein 244 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 255 Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala 266 1 5 20 25 30 277 278 Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val 279 1 5 30 280 20 25 30 281 1 5 10 282 1 Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly 284 1 1 5 30 285 1 10 285 1 10 286 1 10 287 1 10 288 1 10 289 1 10 290 1 10 2		Asp	Met	Lys	_	Val	Val	Cys	Val	Asp	Gln	Gln	Thr	Pro		Ile	Pro	
ALC CGG CTG GCT GCA GAC CCG GTC CTC TCA GGC CTA GCT CAG ATG ATG					440					445					450			
216		220	aaa	ama	COM	CCA	axa	aaa	ama	ama	ma s	aaa	cim s	a a m	ana	A MCI	A THICK	1606
217 218 260 365 360 365 376																		1000
219 CGG GAG TGC TGG TAC CCA AAC CCC TCT GCC CGA CTC ACC GCG CTG CGG 1734			5									- 1						
221	218																	
221																		1734
ATC AAG AAG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA 118 Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro Glu Lys Pro Lys 485 490 495 500 226 CTG ATT CAA TAGCCCAGGA GCACCTGATT CCTTTCTGCC TGCAGGGGGC 1831 228 Val Ile Gln 230 TGGGGGGGTG GGGGGCAGTG GATGGTGCCC TATCTGGGTA GAGGTAGTGT GAGTGTGGTG 1891 231 TGTGCTGGGG ATGGGCAGCT GCGCCTGCCT GCTCGGCCCC CAGCCCACCC AGCCAAAAAT 1951 232 ACAGCTGGGC TGAAACCTGA AAAAAAAAAA AAA 1984 235 (2) INFORMATION FOR SEQ ID NO: 2: (i) SEQUENCE CHARACTERISTICS: ((a) LENGTH: 503 amino acids ((b) TYPE: amino acid ((c) D) TOPOLOGY: linear ((xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 404 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: 415 426 427 438 449 450 450 450 451 452 461 470 471 472 473 474 475 475 476 477 478 479 479 479 479 479 479	_	Arg		Cys	Trp	Tyr	Pro		Pro	Ser	Ala	Arg		Thr	Ala	Leu	Arg	
ATC ANG ANG ACA CTA CAA AAA ATT AGC AAC AGT CCA GAG AAG CCT AAA 1782			470					475					480					
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SEQUENCE VERIFICATION REPORT PATENT APPLICATION US/08/436,265

DATE: 03/12/97 TIME: 14:53:22

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Original Text

29

Wrong Classification

(C) CLASSIFICATION: 514